

Figure 1

10	30	50
CACCGCGTCCGGCGGGCGGGCGGAGAACCCCGCAATCTTGCGCCCACAAAATACACCGA		
70	90	110
CGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC		
130	150	170
CCTACCGCCATGGAACAACGGGGACAGAACGCCCGGCCGCTCGGGGCCGGAAAAGG		
M E Q R G O N A P A A S G A R K R		
190	210	230
CACGGCCCAGGACCCAGGGAGGCCAGGGAGGCCAGGCCCTGGGCCCGGGTCCCCAAGACC		
H G P G P R E A R G A R P G P R V P K T		
250	270	290
CTTGTGCTCGTTGTCGCCGCGCTCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC		
L V L V V A A V L L L V S A E S A L I T		
310	330	350
CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCAACAACAAAAGAGGTCCAGCCCCCTCA		
Q Q D L A P Q Q R A A P Q Q K R S S P S		
370	390	410
GAGGGATTGTGTCACCTGGACACCATATCTCAGAAGACGGTAGAGAGATTGCATCTCCTGC		
E G L C P P G H H I S E D G R D C I S C		
430	450	470
AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTCTGCTTGCCTGCACC		
K Y G Q D Y S T H W N D L L F C L R C T		
490	510	530
AGGTGTGATTCAAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT		
R C D S G E V E L S P C T T T R N T V C		
550	570	590
CAGTGCAGAAAGGCACCTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAAGTGCCGC		
Q C E E G T F R E E D S P E M C R K C R		
610	630	650
ACAGGGTGTCCCAGAGGGATGGTCAAGGTGGTGATTGTACACCCCTGGAGTGACATCGAA		
T G C P R G M V K V G D C T P W S D I E		
670	690	710
TGTGTCCACAAAGAATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT		
C V H K E S G I I G V T V A A V V L I		
730	750	770
GTGGCTGTGTTGTTGCAAGTCTTACTGTGGAAGAAAGTCCTCCTTACCTGAAAGGC		
V A V F V C K S L L W K K V L P Y L K G		
790	810	830
ATCTGCTCAGGTGGTGGGGACCCCTGAGCGTGTGGACAGAACGCTCACAAACGACCTGGG		
I C S G G G D P E R V D R S S Q R P G		
850	870	890
GCTGAGGACAATGTCCTCAATGAGATCGTGAATCTTGCAAGCCCACCCAGGTCCCTGAG		
A E D N V L N E I V S I L Q P T Q V P E		
910	930	950
CAGGAAATGGAAGTCCAGGAGCCAGCAGGCCAACAGGTGTCAACATGTTGCCCGGG		
Q E M E V Q E P A E P T G V N M L S P G		
970	990	1010
GAGTCAGAGCATCTGCTGGAACCGGCAGAACAGGTCTCAGAGGAGGAGGCTGCTG		
E S E H L L E P A E A E R S Q R R R L L		
1030	1050	1070

Figure 1 (continued)

GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA  
V P A N E G D P T E T L R Q C F D D F A  
1090 1110 1130  
GACTTGGTGCCCTTGACTCCTGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT  
D L V P F D S W E P L M R K L G L M D N  
1150 1170 1190  
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGCCACAGGGACACCTTGTACACGATGCTG  
E I K V A K A E A A G H R D T L Y T M L  
1210 1230 1250  
ATAAAAGTGGGTCAAACAAAACGGGCGAGATGCCCTGTCCACACCCCTGCTGGATGCCCTG  
I K W V N K T G R D A S V H T L L D A L  
1270 1290 1310  
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTGAGCTCTGGA  
E T L G E R L A K Q K I E D H L L S S G  
1330 1350 1370  
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCTAAAGTGTGATTCTCTCA  
K F M Y L E G N A D S A M S \*  
1390 1410 1430  
GGAAGTGAGACCTTCCCTGGTTACCTTTCTGGAAAAAGCCCAACTGGACTCCAGTC  
1450 1470 1490  
AGTAGGAAAGTGCCACAATTGTACATGACCGGTACTGGAAGAAACTCTCCATCCAACA  
1510 1530 1550  
TCACCCAGTGGATGGAACATCCTGTAACTTTCACTGCACTTGGCATTATTTTATAAGC  
1570 1590  
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAAA

Figure 2

1	M - L G - - - - -	I W T L L P L U L L	h Fas protein
1	H G L S - - - - -	T V P D L L L P L	h TNFR I Protein
1	H E Q R - - - - -	P R G C A A V A A	DR3 protein
1	M E Q R G Q N A P A A S G A R K R H G P G P R E A R G A R P G P R V P K T L V L	HLYBX88XXprotein	
13	T S V R R L S S K S V N A Q V T D I N S K G L E L R K T V T V E T Q N L E G L	h Fas protein	
14	Y E L L E L V G I Y P S G V I G L V P H E G D R E K R D S V C P Q G K Y I H	h TNFR I Protein	
14	A E L L E L V L G A R A Q G - - - - -	G T R S D R - C D C A - G D F - H - -	DR3 protein
41	V V A A V E L L V S A E S A L I T Q Q D E A P Q Q R H A A P Q Q K R S S P S E G L	HLYBX88XXprotein	
53	H E D G Q E C H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K E Y T	h Fas protein	
52	P Q N N S I C C T K C H K G T V L Y N D C P G P Q D T D C R E C E S G S F T A	h TNFR I Protein	
41	K X I G L F E C C R G C P A G H Y L K A B C T E P C G N S T C L V C P Q D T F L A	DR3 protein	
81	- - - - - C P P G H H I S E D - - - - - G R D C I S C K Y G Q D Y S	HLYBX88XXprotein	
93	D K A H F S S K C R R C R L C D E G H G L E V E I N C T R T Q N T K C R C K P N	h Fas protein	
92	S E N H L 2 - H C L S C S K C R K E M G Q V E I S S C T V D R D T V C G C R K N	h TNFR I Protein	
81	W E N H H W N S E C A R C Q A C D E Q A S O V A L E N C S A V A D T R C G C K P G	DR3 protein	
105	T H W N D L L F C L R C T R C D - S G E V E L S P C T T T R N T V C Q C E E G	HLYBX88XXprotein	
133	F H - - - - - C N S T V - - - C E H C D P C T K - - - - -	h Fas protein	
131	Q Y R E Y W S E N L F Q C - - - F N C S L C L N - G T V H - - - L S C Q E	h TNFR I Protein	
121	W F V E C - - - Q V S O C V S S S B E Y C Q P C L D C G A L H R H T R L L C S R	DR3 protein	
143	T S R E - - - - - E D S P E M C R K C - - - - - R T G C P R	HLYBX88XXprotein	
149	- - - - - C E H G L I - - - K E C - - - - - T L T S N T K C K E - - -	h Fas protein	
161	K Q N T V C T C H A G F F L R E N E C V S C S N C K K S L E C T H L C L P Q I E	h TNFR I Protein	
158	R D T D C G T C L P B G E Y E H G D G C V S C P T S T L G - S C P E R C A A V C G	DR3 protein	
163	G M V K Y G D C T P - - - W S D I E C V - - - - - H R E S G I I E G	HLYBX88XXprotein	
168	- - - - - S G S R S N L G W - - - - - E C L L - L L P I P F L I V - - - - - W	h Fas protein	
201	W V K G T E D S G T T V L E P L V I F F G L C L E S L L F I G E L M Y R V Q R - W	h TNFR I Protein	
197	W R Q - - - - - K F W V Q V L L A G L V V V P L E G A T L T Y T Y R H C W	DR3 protein	
189	- - - - - V T V A A V V E I V A V F - - - V C K S L E W K K V L P Y L K G I C S	HLYBX88XXprotein	
190	V H R R E W Q K E C R R H E K B N Q G S H E S - - - - -	h Fas protein	
240	- H S R L Y S I V C G R S T P B K Z G E L E G T T T K P L A P N P S F S P T P G	h TNFR I Protein	
229	- P H R P L - V E A D E A G M E A L T P P A T H L S P L D S A K T L L A P P D	DR3 protein	
221	- - - - - G G G G D P E R V D R S S Q R P G A E D N V L N E I V S I L Q P T Q	HLYBX88XXprotein	
213	- - - - -	h Fas protein	
279	F T P T L G F S P V B S S T F T S S S T Y T P G D - C P N F A A P R R R E V A P P	h TNFR I Protein	
267	S S E K I C T V Q L V G N S W E P G Y P E T Q E A L C P Q V T W S W D Q E - - P	DR3 protein	
255	V P B Q E M E V O E P A E - - - - - P T G V N M L S P G - - - E S E H E - - -	HLYBX88XXprotein	
213	- - - - - P T L N P E T V A I N E - - - S D V D L S K Y I T T I A G V M	h Fas protein	
313	Y Q G A D B I L A C A L A S D P I P N P L Q K W E D S A H K P Q S L D T D D D P A	h TNFR I Protein	
305	S R A L G B A A A P T L S B - - - - - E S P A G S P A M M L Q P G P Q	DR3 protein	
283	- - - - - L E P A E A E R S Q R R R L L V P A N E G D P T E T L R Q	HLYBX88XXprotein	
241	T E S Q V - - - - - R G F V R K N G V N E A K I D E I K N D N V Q D T A	h Fas protein	
352	T R Y A V V E N V E P P E R W K E F V R R L G L S D H E I D R L I E L Q N G R C L R	h TNFR I Protein	
335	- L Y D V M D A V P A R R W K E F V R C L G L R E A E I E A V E V E I G R - F R	DR3 protein	
312	C E D D F A D I V P F D S W E P L M E K L G L M D N E I - K V A K A E A A G H R	HLYBX88XXprotein	
272	E O K V Q L L R N W H O L E H G K K E A - Y D T L I K D E K K A N L C T L A E K I	h Fas protein	
392	E A Q V S W L A T H R R R T P E R E A T C E L E G R V L R D M D L L G C L E D T	h TNFR I Protein	
373	D C O Y E M I K R W R Q Q P - - - A G L G A V Y A A L E R M G L D G C V E D L	DR3 protein	
351	E T L V T W L I K E V V N K E G F - D A S V H T L L D A L E T L G E R L A K Q K I	HLYBX88XXprotein	
311	Q T I I E K D I T S D S E N S N F R N E I Q S E V	h Fas protein	
433	E E A E - - - - - C G P A A L P P A P S L E R	h TNFR I Protein	
418	- - - - - R S R L Q R G E	DR3 protein	
392	E D H E L S S G K F M Y L E G M - - A D S A M S	HLYBX88XXprotein	

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 3

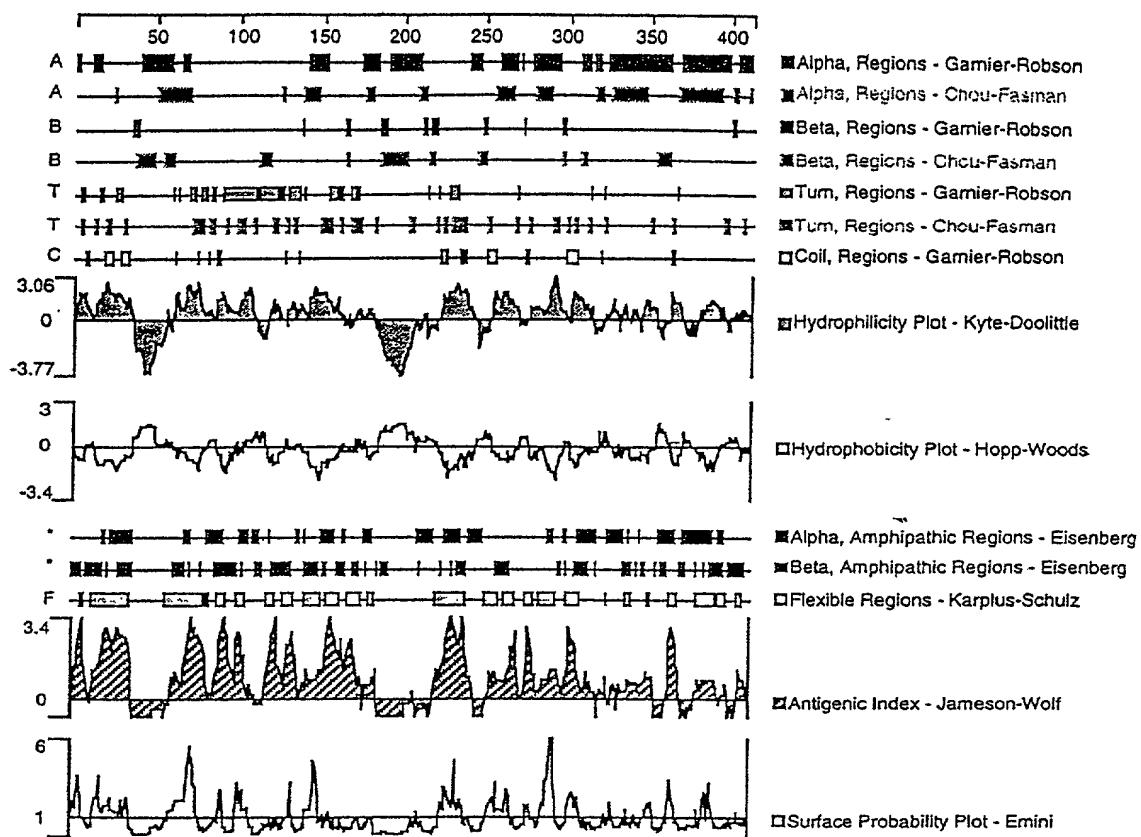


Figure 4

HAPBU13R

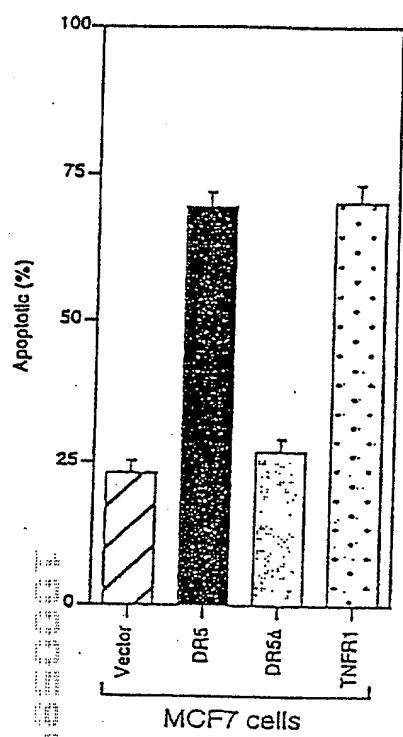
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101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG  
151 GNATGGAAC ACTGATGAAC TTTCACTGC ACTTGGCATT ATTTTGTNA  
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG  
251 TTGTGCGTAC TTTGAGATTG GNGTTGGGG ATGTNCATTG TGTTTGACAG  
301 CACTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG  
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT  
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTGG GTGGGGGGT  
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA  
501 ANNNTGG

HSBBU76R

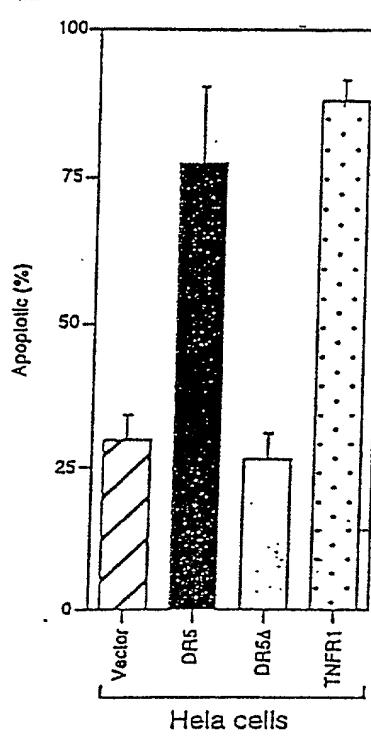
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51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAAATGACA TCCCAAACCA  
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTG CATAGNGTCC  
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201 ACAGGATGTT CCATCCACTG GGTGGATT

Figure 5

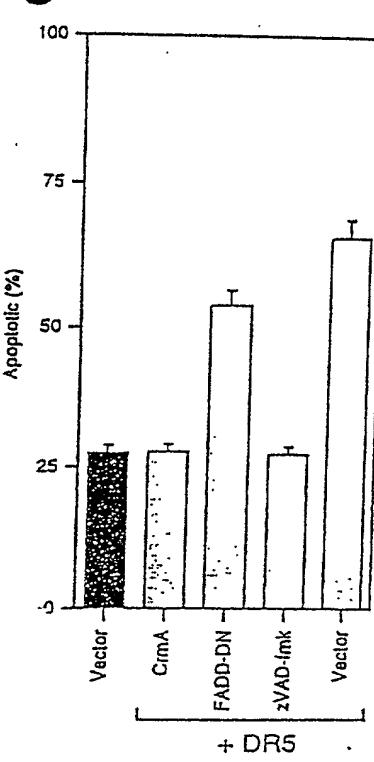
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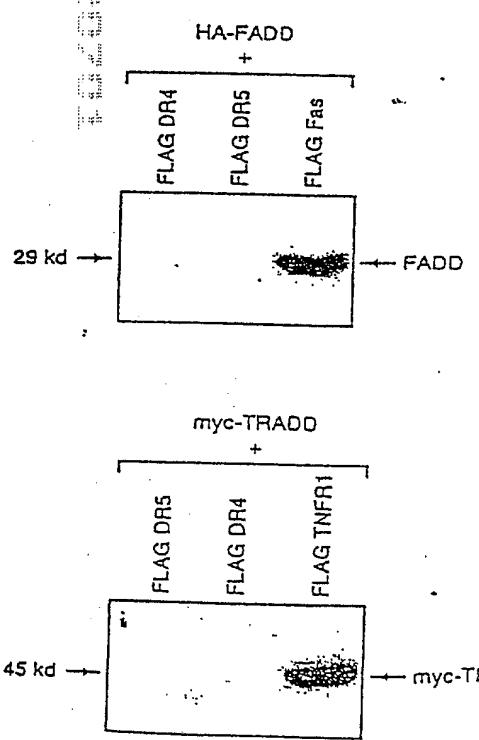
B



C



D



E

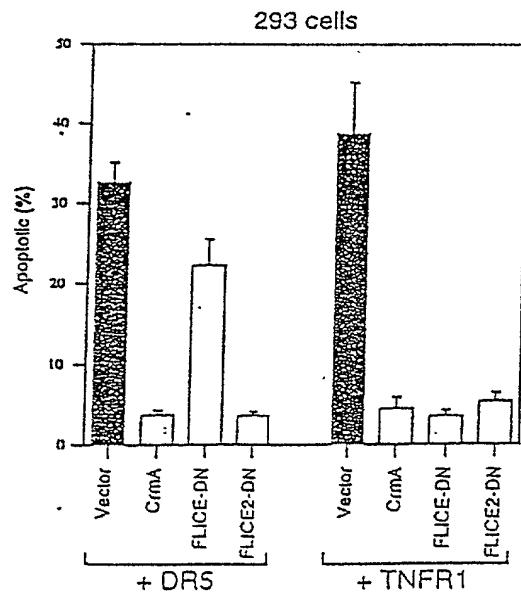
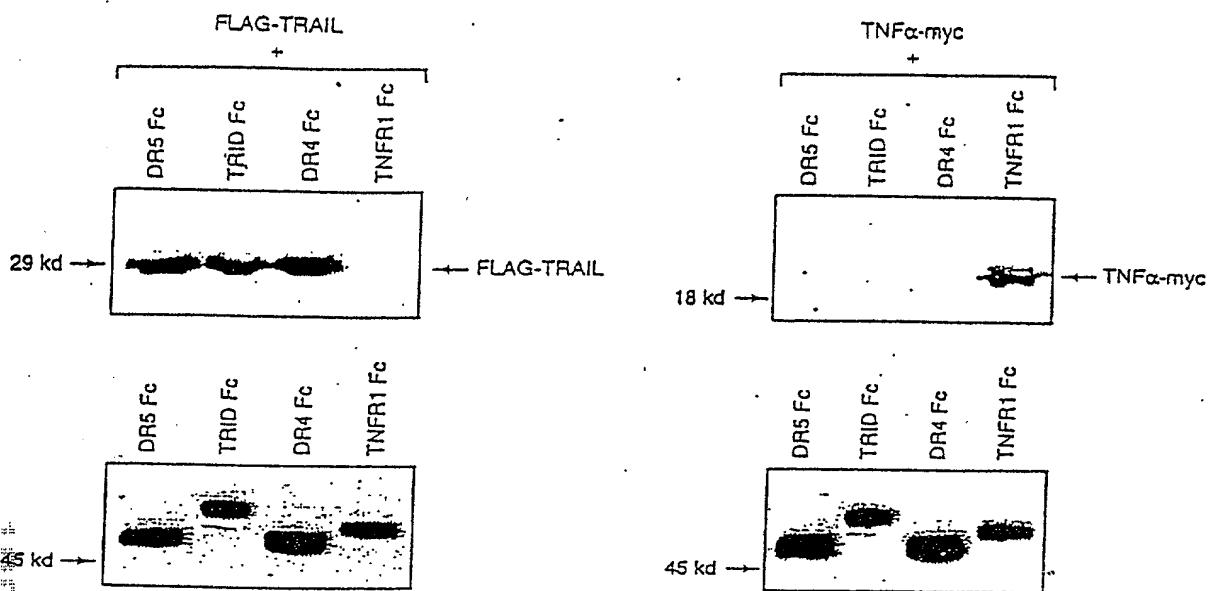


Figure 6

A



C

